IN THE SPECIFICATION:

Please amend Paragraph 0024 to read:

[0024] A number of new microorganisms within the scope of the present invention were deposited on March 13, 2002, with the American Type Culture Collection (hereinafter "ATCC") in accordance with the provisions of the Budapest Treaty on the International Recognition of the Deposit Microorganisms for the Purpose of Patent Procedure. The ATCC is located at 10801 University Boulevard, Manassas, Va. 20110-2209 U.S.A. The deposited microorganisms have been assigned ATCC Designation Nos. PTA-4110, PTA-4111 and ATCC 66669. For purposes of this disclosure, the microorganisms deposited with the ATCC and the ATCC Designation Nos. PTA-4110, PTA-4111 and ATCC 66669 are hereby incorporated by reference. These microorganisms were identified by the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH, and the results of their report are shown in Tables I and II.

<u>Table I</u> <u>Properties of the Strain</u>

Shape of cells	<u>rods</u>
width µm	0.7-0.
length µm	1.5-3.
Pigments	· _
Flagella	+
	
Gram reaction	_ '
	. +
Aminopeptidase (Cerny)	+
Catalase activity	+
Oxidase activity	+
ADH	-
Hydrolysis of gelatin	•
esculin	
•	
	+
DNA	
NO ₂ from NO ₃ (24 th)	
Denitrification	• -
Utilization of	
m-hydrox-benzoat	4
α-amylamin	+
glucose	+
- 0	

citrat	·	 +
malat		+
arabinosse		+
mannose		<u>+</u>
mannit	<u> </u>	<u> </u>
adipat		
caprat	<u> </u>	+
gluconat		<u>+</u>
maltose		
citraconat		=
itaconat		<u> </u>
inositol		+
mesaconat		+
butandiol		
tryptamin		
butylamin		
L-arabitol		
rhamnose		+
L-alanin	<u> </u>	+
melibiose		=

Result: = Burkholderia sp.

The partial sequencing of the 16SrDNA shows a similarity of around 97% to several species of the genus Burkholderia.

The profile of the cellular fatty acids is typical for the Burkholderia-group.

The results of the physiological tests do not allow a complete identification of this strain. They point to *B. cepacia*.

Considering all these results, especially the result of the partial sequencing, this strain may be a member of a new species within this genus.

<u>Table II</u> <u>Fatty Acid Profile</u>

RT _	Area	Ar/Ht	Respon	ECL	Name	%	Comment 1	Comment 2
	308111640	0.037	TCHEST	7.000	SOLVENT PEAK	•••	< min rt	
	755	0.037		7.551			< min rt	
2.060	600	0.036	1.077		Sum in Feature 2	0.17	ECL deviates	-0.003 unknown 10.928
4.046		0.045	1.012		13:1 AT 12-13	0.40	ECL deviates	
6.183		0.040	0.988	14.001	14:0	3.65	ECL deviates	0.001 Reference -0.004
7,663		0.040	0.973	14.861	15:1 w6c	0.42	ECL deviates	0.005
9.015		0.067	0.971	14.998		0.37		-0.002 Reference -0.007
9.231		0.045	0.965	15.490	Sum in Feature 2	4.75	ECL deviates	0.002 14:0 30H/16:1 ISO I
10.061	80640		0.960	15.821	Sum in Feature 3	20.60	ECL deviates	-0.001 16:1 w7c/15 iso 20H
10.620		0.045	0.958		16:0	19.73	ECL deviates	0.001 Reference -0.005
10.924		0.040	0.950	16.889	17:0 CYCLO		ECL deviates	0.001 Reference -0.004
12.479		0.031	0.949	17,000	17:0	0.24	ECL deviates	-0.000 Reference -0.006
12,672 12,762		0.041	0.949	17.051	16:1 20H		ECL deviates	0.003
13.089		0.050	0.947	17,235	16:0 20H	1.06	ECL deviates	0.002
13.592		0.049	0.945	17,520	16:0 30H	3.62	ECL deviates	<u> 0.001</u>
14.136	154907		0.943	17.827	18:1 w7c		ECL deviates	0.004
14.440		0.047	0.942	17.998	18:0			-0.002 Reference -0.006
14,586		0.052	0.941	18.081	11 methyl 18:1 w7	c 0.21	ECL deviates	<u>-0.000</u>
16.033		0.051	0.936	18.90 <u>3</u>	19:0 CYCLO w8c			0,001 Reference -0.003
16.362		0.060	0.935	19.090	18:1 20H		ECL deviates	0.001
17.655	948	0.086	0.931	19.834	20:1 w7c		ECL deviates	0.003
*****	19111				Summed Feature 2	<u>4.92</u>	12:0 ALDE?	unknown 10.928
*****		-	<u></u>		<u> </u>			0 30H 14:0 30H/16:1 ISO I
*****	80640) <u>, , . , .</u>	<u> </u>		Summed Feature 3	20.60	16:1 w7c/15 is	o 20H 15:0 ISO 20H/16:1w7c
			•					n engr ctio
Solvent A	r Total Are	a Nam	ed Area	% Name	d Total Amut Nbr	<u>Ref E</u>	CL Deviation	Ref ECL Smit
30811164			394649	100,00	376057	7	0.002	0.005
							0.060 (Decords	omerica conacia)
	TSBA40 [I	Rev 4.10						omonas cepacia)
	B. cepacia							
	B. c, GC subgroup B*							
	B. c. GC subgroup A*							
	B. pyrrocinia**					0.624 (Pseudomonas glathei)		

B. glathei**